

FIG. 1

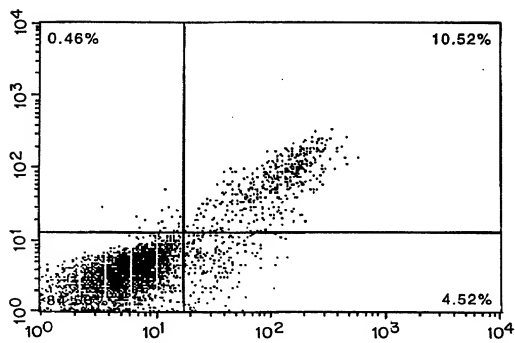


FIG. 2

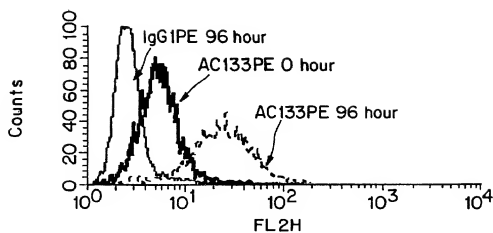


FIG. 3

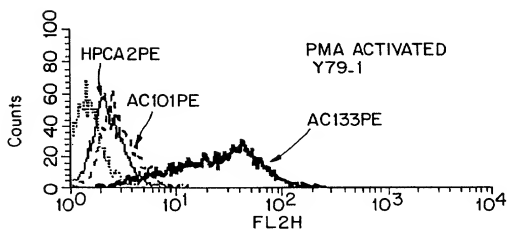


FIG.4A

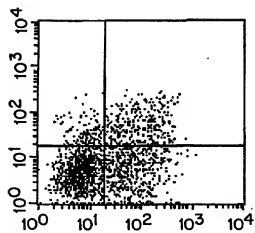


FIG.4B

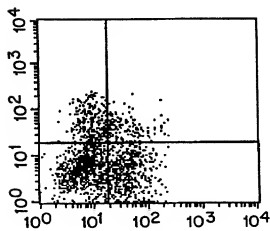


FIG.5A

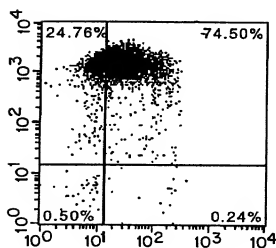


FIG.5B

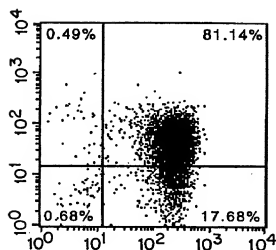


FIG.5C

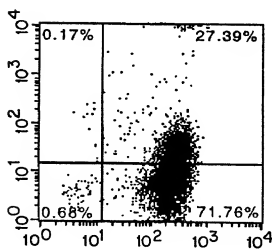


FIG.5D

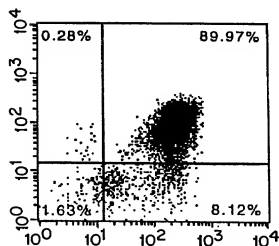


FIG.6

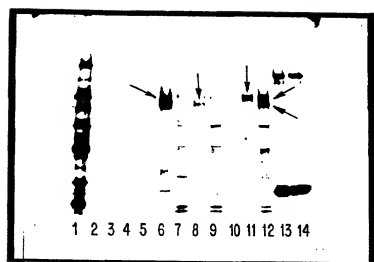


FIG. 7A

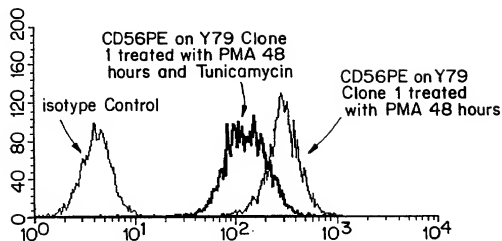


FIG. 7B

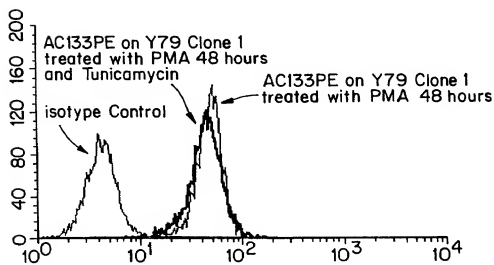
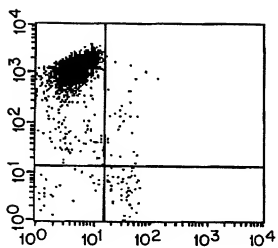


FIG.8



00004573 = 01301

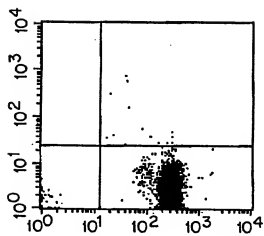


FIG.9B

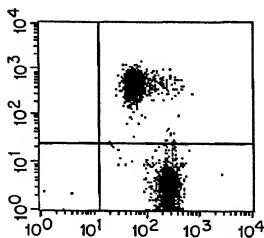
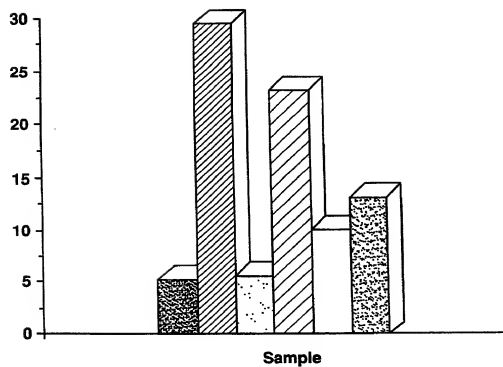


FIG.10



- LP Control/CFU-GM
- ▨ LP Control/BFU-E
- ▩ C4-AC101/CFU-GM
- ▧ C4-AC101/BFU-E
- C4-AC133/CFU-GM
- ▦ C4-AC133/BFU-E

FIG.11

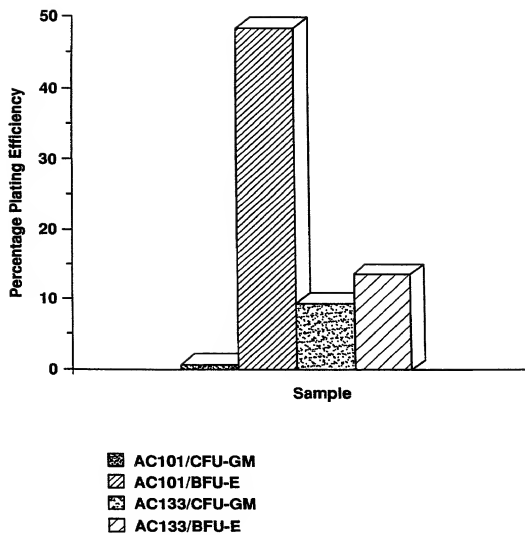


FIG.12 -1

CCAAGTCTCA CCTCATGTTT GGAGGATCTT GCTAGCT	ATG GCC CTC GTA CTC GGC	55
	Met Ala Leu Val Leu Gly	
	1 5	
TCC CTG TTG CTG CTG GGG CTG TGC GGG AAC TCC TTT TCA GGA GGG CAG		103
Ser Leu Leu Leu Leu Gly Leu Cys Gly Asn Ser Phe Ser Gly Gly Gln		
	10 15 20	
CCT TCA TCC ACA GAT GCT CCT AAG GCT TGG AAT TAT GAA TTG CCT GCA		151
Pro Ser Ser Thr Asp Ala Pro Lys Ala Trp Asn Tyr Glu Leu Pro Ala		
	25 30 35	
ACA AAT TAT GAG ACC CAA GAC TCC CAT AAA GCT GGA CCC ATT GGC ATT		199
Thr Asn Tyr Glu Thr Gln Asp Ser His Lys Ala Gly Pro Ile Gly Ile		
	40 45 50	
CTC TTT GAA CTA GTG CAT ATC TTT CTC TAT GTG GTA CAG CCG CGT GAT		247
Leu Phe Glu Leu Val His Ile Phe Leu Tyr Val Val Gln Pro Arg Asp		
	55 60 65 70	
TTC CCA GAA GAT ACT TTG AGA AAA TTC TTA CAG AAG GCA TAT GAA TCC		295
Phe Pro Glu Asp Thr Leu Arg Lys Phe Leu Gln Lys Ala Tyr Glu Ser		
	75 80 85	
AAA ATT GAT TAT GAC AAG CCA GAA ACT GTA ATC TTA GGT CTA AAG ATT		343
Lys Ile Asp Tyr Asp Lys Pro Glu Thr Val Ile Leu Gly Leu Lys Ile		
	90 95 100	
GTC TAC TAT GAA GCA GGG ATT ATT CTA TGC TGT GTC CTG GGG CTG CTG		391
Val Tyr Tyr Glu Ala Gly Ile Ile Leu Cys Cys Val Leu Gly Leu Leu		
	105 110 115	
TTT ATT ATT CTG ATG CCT CTG GTG GGG TAT TTC TTT TGT ATG TGT CGT		439
Phe Ile Ile Leu Met Pro Leu Val Gly Tyr Phe Phe Cys Met Cys Arg		
	120 125 130	
TGC TGT AAC AAA TGT GGT GGA GAA ATG CAC CAG CGA CAG AAG GAA AAT		487
Cys Cys Asn Lys Cys Gly Gly Glu Met His Gln Arg Gln Lys Glu Asn		
	135 140 145 150	
GGG CCC TTC CTG AGG AAA TGC TTT GCA ATC TCC CTG TTG GTG ATT TGT		535
Gly Pro Phe Leu Arg Lys Cys Phe Ala Ile Ser Leu Leu Val Ile Cys		
	155 160 165	
ATA ATA ATA AGC ATT GGC ATC TTC TAT GGT TTT GTG GCA AAT CAC CAG		583
Ile Ile Ile Ser Ile Gly Ile Phe Tyr Gly Phe Val Ala Asn His Gln		
	170 175 180	
GTA AGA ACC CGG ATC AAA AGG AGT CGG AAA CTG GCA GAT AGC AAT TTC		631
Val Arg Thr Arg Ile Lys Arg Ser Arg Lys Leu Ala Asp Ser Asn Phe		
	185 190 195	
AAG GAC TTG CGA ACT CTC TTG AAT GAA ACT CCA GAG CAA ATC AAA TAT		679
Lys Asp Leu Arg Thr Leu Asn Glu Thr Pro Glu Gln Ile Lys Tyr		
	200 205 210	
ATA TTG GCC CAG TAC AAC ACT ACC AAG GAC AAG GCG TTC ACA GAT CTG		727
Ile Leu Ala Gln Tyr Asn Thr Thr Lys Asp Lys Ala Phe Thr Asp Leu		
	215 220 225 230	

FIG.12-2

AAC AGT ATC AAT TCA GTG CTA GGA GGC GGA ATT CTT GAC CGA CTG AGA Asn Ser Ile Asn Ser Val Leu Gly Gly Gly Ile Leu Asp Arg Leu Arg	775
235	
CCC AAC ATC ATC CCT GTT CTT GAT GAG ATT AAG TCC ATG GCA ACA GCG Pro Asn Ile Ile Pro Val Leu Asp Asp Ile Lys Ser Met Ala Thr Ala	823
250	
255	
260	
ATC AAG GAG ACC AAA GAG GCG TTG GAG AAC ATG AAC AGC ACC TTG AAG Ile Lys Glu Thr Lys Glu Ala Leu Glu Asn Met <u>Asn Ser Thr</u> Leu Lys	871
265	
270	
275	
AGC TTG CAC CAA CAA AGT ACA CAG CTT AGC AGC AGT CTG ACC AGC GTG Ser Leu His Gln Gln Ser Thr Gln Leu Ser Ser Ser Leu Thr Ser Val	919
280	
285	
290	
AAA ACT AGC CTG CGG TCA TCT CTC AAT GAC CCT CTG TGC TTG GTG CAT Lys Thr Ser Leu Arg Ser Ser Leu Asn Asp Pro Leu Cys Leu Val His	967
295	
300	
305	
310	
CCA TCA AGT GAA ACC TGC AAC AGC ATC AGA TTG TCT CTA AGC CAG CTG Pro Ser Ser Glu Thr Cys Asn Ser Ile Arg Leu Ser Leu Ser Gln Leu	1015
315	
320	
325	
AAT AGC AAC CCT GAA CTG AGG CAG CTT CCA CCC GTG GAT GCA GAA CTT Asn Ser Asn Pro Glu Leu Arg Gln Leu Pro Pro Val Asp Ala Glu Leu	1063
330	
335	
340	
GAC AAC GTT AAT AAC GTT CTT AGG ACA GAT TTG GAT GGC CTG GTC CAA Asp Asn Val Asn Asn Val Leu Arg Thr Asp Leu Asp Gly Leu Val Gln	1111
345	
350	
355	
CAG GGC TAT CAA TCC CTT AAT GAT ATA CCT GAC AGA GTA CAA CGC CAA Gln Gly Tyr Gln Ser Leu Asn Asp Ile Pro Asp Arg Val Gln Arg Gln	1159
360	
365	
370	
ACC ACG ACT GTC GTA GCA GGT ATC AAA AGG GTC TTG AAT TCC ATT GGT Thr Thr Thr Val Val Ala Gly Ile Lys Arg Val Leu Asn Ser Ile Gly	1207
375	
380	
385	
390	
TCA GAT ATC GAC AAT GTA ACT CAG CGT CTT CCT ATT CAG GAT ATA CTC Ser Asp Ile Asp <u>Asn Val Thr</u> Gln Arg Leu Pro Ile Gln Asp Ile Leu	1255
395	
400	
405	
TCA GCA TTC TCT GTT TAT GTT AAT AAC ACT GAA AGT TAC ATC CAC AGA Ser Ala Phe Ser Val Tyr Val <u>Asn Asn Thr</u> Glu Ser Tyr Ile His Arg	1303
410	
415	
420	
AAT TTA CCT ACA TTG GAA GAG TAT GAT TCA TAC TGG TGG CTG GGT GGC Asn Leu Pro Thr Leu Glu Glu Tyr Asp Ser Tyr Trp Trp <u>Leu Gly Gly</u>	1351
425	
430	
435	
CTG GTC ATC TGC TCT CTG CTG ACC CTC ATC GTG ATT TTT TAC TAC CTG Leu Val Ile Cys Ser Leu Leu Thr Leu Ile Val Ile Phe Tyr Tyr Leu	1399
440	
445	
450	
GGC TTA CTG TGT GGC GTG TGC GGC TAT GAC AGG CAT GCC ACC CCG ACC Gly Leu Leu Cys Gly Val Cys Gly Tyr Asp Arg His Ala Thr Pro Thr	1447
455	
460	
465	
470	

FIG.12-3

ACC CGA GGC TGT GTC TCC AAC ACC GGA GGC GTC TTC CTC ATG GTT GGA Thr Arg Gly Cys Val Ser Asn Thr Gly Gly Val Phe Leu Met Val Gly	1495
475 480 485	
GTT GGA TTA AGT TTC CTC TTT TGC TGG ATA TTG ATG ATC ATT GTG GTT Val Gly Leu Ser Phe Leu Phe Cys Trp Ile Leu Met Ile Ile Val Val	1543
490 495 500	
CTT ACC TTT GTC TTT GGT GCA AAT GTG GAA AAA CTG ATC TGT GAA CCT Leu Thr Phe Val Phe Gly Ala Asn Val Glu Lys Leu Ile Cys Glu Pro	1591
505 510 515	
TAC ACG AGC AAG GAA TTA TTC CGG GTT TTG GAT ACA CCC TAC TTA CTA Tyr Thr Ser Lys Glu Leu Phe Arg Val Leu Asp Thr Pro Tyr Leu Leu	1639
520 525 530	
AAT GAA GAC TGG GAA TAC TAT CTC TCT GGG AAG CTA TTT AAT AAA TCA Asn Glu Asp Trp Glu Tyr Tyr Leu Ser Gly Lys Leu Phe Asn Lys Ser	1687
535 540 545 550	
AAA ATG AAG CTC ACT TTT GAA CAA GTT TAC AGT GAC TGC AAA AAA AAT Lys Met Lys Leu Thr Phe Glu Gln Val Tyr Ser Asp Cys Lys Lys Asn	1735
555 560 565	
AGA GGC ACT TAC GGC ACT CTT CAC CTG CAG AAC AGC TTC AAT ATC AGT Arg Gly Thr Tyr Gly Thr Leu His Leu Gln Asn Ser Phe Asn Ile Ser	1783
570 575 580	
GAA CAT CTC AAC ATT AAT GAG CAT ACT GGA AGC ATA AGC AGT GAA TTG Glu His Leu Asn Ile Asn Glu His Thr Gly Ser Ile Ser Ser Glu Leu	1831
585 590 595	
GAA AGT CTG AAG GTA AAT CTT AAT ATC TTT CTG TTG GGT GCA GCA GGA Glu Ser Leu Lys Val Asn Leu Asn Ile Phe Leu Leu Gly Ala Ala Gly	1879
600 605 610	
AGA AAA AAC CTT CAG GAT TTT GCT GCT TGT GGA ATA GAC AGA ATG AAT Arg Lys Asn Leu Gln Asp Phe Ala Ala Cys Gly Ile Asp Arg Met Asn	1927
615 620 625 630	
TAT GAC AGC TAC TTG GCT CAG ACT GGT AAA TCC CCC GCA GGA GTG AAT Tyr Asp Ser Tyr Leu Ala Gln Thr Gly Lys Ser Pro Ala Gly Val Asn	1975
635 640 645	
CTT TTA TCA TTT GCA TAT GAT CTA GAA GCA AAA GCA AAC AGT TTG CCC Leu Leu Ser Phe Ala Tyr Asp Leu Glu Ala Lys Ala Asn Ser Leu Pro	2023
650 655 660	
CCA GGA AAT TTG AGG AAC TCC CTG AAA AGA GAT GCA CAA ACT ATT AAA Pro Gly Asn Leu Arg Asn Ser Leu Lys Arg Asp Ala Gln Thr Ile Lys	2071
665 670 675	
ACA ATT CAC CAG CAA CGA GTC CTT CCT ATA GAA CAA TCA CTG AGC ACT Thr Ile His Gln Gln Arg Val Leu Pro Ile Glu Gln Ser Leu Ser Thr	2119
680 685 690	
CTA TAC CAA AGC GTC AAG ATA CTT CAA CGC ACA GGG AAT GGA TTG TTG Leu Tyr Gln Ser Val Lys Ile Leu Gln Arg Thr Gly Asn Gly Leu Leu	2167
695 700 705 710	
GAG AGA GTA ACT AGG ATT CTA GCT TCT CTG GAT TTT GCT CAG AAC TTC Glu Arg Val Thr Arg Ile Leu Ala Ser Leu Asp Phe Ala Gln Asn Phe	2215
715 720 725	

FIG.12-4

ATC ACA AAC AAT ACT TCC TCT GTT ATT ATT GAG GAA ACT AAG AAG TAT Ile Thr <u>Asn;Asn Thr;Ser</u> Ser Val Ile Ile Glu Glu Thr Lys Lys Tyr 730 735 740	2263
GGG AGA ACA ATA ATA GGA TAT TTT GAA CAT TAT CTG CAG TGG ATC GAG Gly Arg Ser Ile Ile Gly Tyr Phe Glu His Tyr Leu Gln Trp Ile Glu 745 750 755	2311
TTC TCT ATC AGT GAG AAA GTG GCA TCG TGC AAA CCT GTG GCC ACC GCT Phe Ser Ile Ser Glu Lys Val Ala Ser Cys Lys Pro Val Ala Thr Ala 760 765 770	2359
CTA GAT ACT GCT GTT GAT GTC TTT CTG TGT AGC TAC ATT ATC GAC CCC Leu Asp Thr Ala Val Asp Val Phe Leu Cys Ser Tyr Ile Ile Asp Pro 775 780 785	2407
TTG AAT TTG TTT TGG TTT GGC ATA GGA AAA GCT ACT GTA TTT TTA CTT Leu Asn <u>Leu Phe Trp</u> Phe Gly Ile Gly Lys Ala Thr Val Phe Leu Leu 795 800 805	2455
CCG GCT CTA ATT TTT GCG GTA AAA CTG GCT AAG TAC TAT CGT CGA ATG Pro Ala Leu <u>Ile Phe</u> Ala Val Lys Leu Ala Lys Tyr Tyr Arg Arg Met 810 815 820	2503
GAT TCG GAG GAC GTG TAC GAT GAT GTT GAA ACT ATA CCC ATG AAA AAT Asp Ser Glu Asp Val Tyr Asp Asp Val Glu Thr Ile Pro Met Lys Asn 825 830 835	2551
ATG GAA AAT GGT AAT AAT GGT TAT CAT AAA GAT CAT GTA TAT GGT ATT Met Glu Asn Gly Asn Asn Gly Tyr His Lys Asp His Val Tyr Gly Ile 840 845 850	2599
CAC AAT CCT GTT ATG ACA AGC CCA TCA CAA CAT T GATAGCTGAT His Asn Pro Val Met Thr Ser Pro Ser Gln His 855 860	2643
GTTGAAACTG CTGAGCATC AGGATACTCA AAGTGGAAG GATCACAGAT TTTTGGTAGT	2703
TTCTGGGTCT ACAAGGACTT TCCAAATCCA GGAGCAACGC CAGTGGCAAC GTAGTGACTC	2763
AGGCGGGCAC CAAGGCAACG GCACCATTGG TCTCTGGGTA GTGCTTTAAG AATGAACACA	2823
ATCACGTTAT AGTCCATGGT CCATCACTAT TCAAGGATGA CTCCTCCCTC TCCTGTCTAT	2883
TTTTGTTTTT TACTTTTTTA CACTGAGTIT CTATTTAGAC ACTACAACAT ATGGGGTGTT	2943
TGTTCCCATTT GGATGCATTT CTATCAAAAC TCTATCAAAT GTGATGGCTA GATTCTAACAA	3003
TATTGCCATG TGTGGAGTGT GCTGAACACA CACCAGTTTA CAGGAAAGAT GCATTTTGTG	3063
TACAGTAAAC GGTGTATATA CCTTTTGTTA CCACAGAGTT TTTTAAACAA ATGAGTATTA	3123
TAGGACTTTC TTCTAAATGA GCTAAATAAG TCACCATTGA CTTCTTGGTG CTGTTGAAAA	3183
TAATCCATTT TCACTAAAAG TGTGTGAAAC CTACAGCATA TTCCTCACGC AGAGATTTTC	3243
ATCTATTATA CTTTATCAAA GATTGGCCAT GTTCCACTTG GAAATGGCAT GCAAAAGCCA	3303
TCATAGAGAA ACCTGCGTAA CTCCACTTGA CAAATTCAAA AGAGAGAGAG AGATCTTGAG	3363
AGAGAAATGC TGTTCGTTCA AAAGTGGAGT TGTITTAACA GATGCCAATT ACGGTGTACA	3423

FIG.12-5

GTTTAACAGA GTTITCTGTT GCATTAGGAT AACATTAAT TGGAGTGCAG CTAACATGAG	3483
TATCATCAGA CTAGTATCAA GTGTTCTAAA ATGAAATATG AGAAGATCCT GTCACAATTC	3543
TTAGATCTGG TGTCCAGCAT GGATGAAACC TTGAGTTTG GTCCTAAAT TTGCATGAAA	3603
GCACAAGGTA AATATTCAAT TGCTTCAGGA GTTTCATGTT GGATCTGTCA TTATCAAAAG	3663
TGATCAGCAA TGAAGAACTG GTCGGACAAA ATTTAACGTT GATGTAATGG AATTCAGAT	3723
GTAGGCATTG CCCCAGGTC TTTTCATGTG CAGATTGCAG TTCTGATTCA TTGATAAAA	3783
AAGGAACTTG GAAAAAAAAA A	3804

FIG.13

